

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2009; month=8; day=14; hr=8; min=9; sec=16; ms=907;]

=====

Application No: 10539723 Version No: 2.0

Input Set:

Output Set:

Started: 2009-07-29 17:34:22.203
Finished: 2009-07-29 17:34:23.082
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 879 ms
Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 10
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

SEQUENCE LISTING

<110> Bayer CropScience GmbH
Hoehne, Michaela
Frohberg, Claus
Landschuetze, Volker

<120> Plant cells and plants which synthesize a starch with an
increased final viscosity

<130> 65084.000013

<140> 10539723
<141> 2005-06-20

<150> EP 02028530.0
<151> 2002-12-19

<150> PCT/EP03/14840
<151> 2003-12-19

<150> EP 03090275.3
<151> 2003-08-29

<160> 10

<170> PatentIn version 3.5

<210> 1

<211> 4167

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (207)..(3899)

<300>

<301> Abel,G.J., Springer,F., Willmitzer,L. and Kossmann,J.

<302> Cloning and functional analysis of a cDNA encoding a novel 139 kDa

<303> Plant J.

<304> 10

<305> 6

<306> 981-991

<307> 1996

<308> X94400

<309> 1995-12-22

<313> (1)..(4167)

<300>

<308> EMBL / X94400

<309> 1997-04-16

<313> (1)..(4167)

<400> 1

ttttttaata gattttttaaa accccattaa agcaaatacg tatataattg cagcacagat 60

acagagagggg agagagaaaag atagtgtgtt gatgaaggag aagagagata tttcacatgg 120

gatgttctat ttgattctgt ggtgaacaag agttttacaa agaacattcc tttttctttt 180

tttcttggtt cttgtgtggg tcagcc atg gat gtt cca ttt cca ctg cat aga 233
Met Asp Val Pro Phe Pro Leu His Arg
1 5

cca ttg agt tgc aca agt gtc tcc aat gca ata acc cac ctc aag atc 281
Pro Leu Ser Cys Thr Ser Val Ser Asn Ala Ile Thr His Leu Lys Ile
10 15 20 25

aaa cct ttt ctt ggg ttt gtc tct cat gga acc aca agt cta tca gta 329
Lys Pro Phe Leu Gly Phe Val Ser His Gly Thr Thr Ser Leu Ser Val
30 35 40

caa tct tct tca tgg agg aag gat gga atg gtt act ggg gtt tca ttt 377
Gln Ser Ser Ser Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe
45 50 55

cca ttt tgt gca aat ctc tcg gga aga aga cgg aga aaa gtt tca act 425
Pro Phe Cys Ala Asn Leu Ser Gly Arg Arg Arg Arg Lys Val Ser Thr
60 65 70

act agg agt caa gga tct tca cct aag ggg ttt gtg cca agg aag ccc 473
Thr Arg Ser Gln Gly Ser Ser Pro Lys Gly Phe Val Pro Arg Lys Pro

75	80	85	
tca ggg atg agc acg	caa aga aag gtt	cag aag agc aat ggt gat aaa	521
Ser Gly Met Ser Thr	Gln Arg Lys Val	Gln Lys Ser Asn Gly Asp Lys	
90	95	100 105	
 gaa agt caa agt act	tca aca tct aaa	gaa tct gaa att tcc aac cag	569
Glu Ser Gln Ser Thr	Ser Thr Ser Lys	Glu Ser Glu Ile Ser Asn Gln	
110	115	120	
 aag acg gtt gaa gca aga	gtt gaa act agt	gac gat gac act aaa gta	617
Lys Thr Val Glu Ala Arg	Val Glu Thr Ser	Asp Asp Asp Thr Lys Val	
125	130	135	
 gtg gtg agg gac cac	aag ttt ctg gag	gat gag gat gaa atc aat ggt	665
Val Val Arg Asp His	Lys Phe Leu Glu	Asp Glu Asp Glu Ile Asn Gly	
140	145	150	
 tct act aaa tca ata agt	atg tca cct gtt	cgt gta tca tct caa ttt	713
Ser Thr Lys Ser Ile Ser	Met Ser Pro Val	Arg Val Ser Ser Gln Phe	
155	160	165	
 gtt gaa agt gaa gaa act	ggg ggt gat gac	aag gat gct gta aag tta	761
Val Glu Ser Glu Glu Thr	Gly Gly Asp Asp	Lys Asp Ala Val Lys Leu	
170	175	180 185	
 aac aaa tca aag aga tcg	gaa gag agt gat	ttt cta att gat tct gta	809
Asn Lys Ser Lys Arg Ser	Glu Glu Ser Asp	Phe Leu Ile Asp Ser Val	
190	195	200	
 ata aga gaa caa agt gga	tct cag ggg gaa act	aat gcc agt agc aag	857
Ile Arg Glu Gln Ser Gly	Ser Gln Gly Glu Thr	Asn Ala Ser Ser Lys	
205	210	215	
 gga agc cat gct gtg ggt	aca aaa ctt tat	gag ata ttg cag gtg gat	905
Gly Ser His Ala Val Gly	Thr Lys Leu Tyr	Glu Ile Leu Gln Val Asp	
220	225	230	
 gtt gag cca caa caa ttg	aaa gaa aat aat	gct ggg aat gtt gaa tac	953
Val Glu Pro Gln Gln Leu	Lys Glu Asn Asn	Ala Gly Asn Val Glu Tyr	
235	240	245	
 aaa gga cct gta gca agt	aag cta ttg gaa att	act aag gct agt gat	1001
Lys Gly Pro Val Ala Ser	Lys Leu Leu Glu	Ile Thr Lys Ala Ser Asp	
250	255	260 265	
 gtg gaa cac act gaa agc	aat gag att gat	gac tta gac act aat agt	1049
Val Glu His Thr Glu Ser	Asn Glu Ile Asp	Asp Leu Asp Thr Asn Ser	
270	275	280	
 ttc ttt aaa tca gat tta	att gaa gag gat	gag cca tta gct gca gga	1097
Phe Phe Lys Ser Asp Leu	Ile Glu Glu Asp	Glu Pro Leu Ala Ala Gly	
285	290	295	
 aca gtg gag act gga gat	tct tct cta aac	tta aga ttg gag atg gaa	1145
Thr Val Glu Thr Gly Asp	Ser Ser Leu Asn	Leu Arg Leu Glu Met Glu	
300	305	310	

gca aat cta cgt agg cag gct ata gaa agg ctt gcc gag gaa aat tta	1193
Ala Asn Leu Arg Arg Gln Ala Ile Glu Arg Leu Ala Glu Glu Asn Leu	
315 320 325	
ttg caa ggg atc aga tta ttt tgt ttt cca gag gtt gta aaa cct gat	1241
Leu Gln Gly Ile Arg Leu Phe Cys Phe Pro Glu Val Val Lys Pro Asp	
330 335 340 345	
gaa gat gtc gag ata ttt ctt aac aga ggt ctt tcc act ttg aag aat	1289
Glu Asp Val Glu Ile Phe Leu Asn Arg Gly Leu Ser Thr Leu Lys Asn	
350 355 360	
gag tct gat gtc ttg att atg gga gct ttt aat gag tgg cgc tat agg	1337
Glu Ser Asp Val Leu Ile Met Gly Ala Phe Asn Glu Trp Arg Tyr Arg	
365 370 375	
tct ttt act aca agg cta act gag act cat ctc aat gga gat tgg tgg	1385
Ser Phe Thr Thr Arg Leu Thr Glu Thr His Leu Asn Gly Asp Trp Trp	
380 385 390	
tct tgc aag atc cat gtt ccc aag gaa gca tac agg gct gat ttt gtg	1433
Ser Cys Lys Ile His Val Pro Lys Glu Ala Tyr Arg Ala Asp Phe Val	
395 400 405	
ttt ttt aat gga caa gat gtc tat gac aac aat gat gga aat gac ttc	1481
Phe Phe Asn Gly Gln Asp Val Tyr Asp Asn Asn Asp Gly Asn Asp Phe	
410 415 420 425	
agt ata act gtg aaa ggt ggt atg caa atc att gac ttt gaa aat ttc	1529
Ser Ile Thr Val Lys Gly Gly Met Gln Ile Ile Asp Phe Glu Asn Phe	
430 435 440	
ttg ctt gag gag aaa tgg aga gaa cag gag aaa ctt gct aaa gaa caa	1577
Leu Leu Glu Glu Lys Trp Arg Glu Gln Glu Lys Leu Ala Lys Glu Gln	
445 450 455	
gct gaa aga gaa aga cta gcg gaa gaa caa aga cga ata gaa gca gag	1625
Ala Glu Arg Glu Arg Leu Ala Glu Glu Gln Arg Arg Ile Glu Ala Glu	
460 465 470	
aaa gct gaa att gaa gct gac aga gca caa gca aag gaa gag gct gca	1673
Lys Ala Glu Ile Glu Ala Asp Arg Ala Gln Ala Lys Glu Glu Ala Ala	
475 480 485	
aag aaa aag aaa gta ttg cga gaa ttg atg gta aaa gcc acg aag act	1721
Lys Lys Lys Lys Val Leu Arg Glu Leu Met Val Lys Ala Thr Lys Thr	
490 495 500 505	
cgt gat atc acg tgg tac ata gag cca agt gaa ttt aaa tgc gag gac	1769
Arg Asp Ile Thr Trp Tyr Ile Glu Pro Ser Glu Phe Lys Cys Glu Asp	
510 515 520	
aag gtc agg tta tac tat aac aaa agt tca ggt cct ctc tcc cat gct	1817
Lys Val Arg Leu Tyr Tyr Asn Lys Ser Ser Gly Pro Leu Ser His Ala	
525 530 535	

aag gac ttg tgg atc cac gga gga tat aat aat tgg aag gat ggt ttg	1865
Lys Asp Leu Trp Ile His Gly Gly Tyr Asn Asn Trp Lys Asp Gly Leu	
540 545 550	
tct att gtc aaa aag ctt gtt aaa tct gag aga ata gat ggt gat tgg	1913
Ser Ile Val Lys Lys Leu Val Lys Ser Glu Arg Ile Asp Gly Asp Trp	
555 560 565	
tgg tat aca gag gtt gtt att cct gat cag gca ctt ttc ttg gat tgg	1961
Trp Tyr Thr Glu Val Val Ile Pro Asp Gln Ala Leu Phe Leu Asp Trp	
570 575 580 585	
gtt ttt gct gat ggt cca ccc aag cat gcc att gct tat gat aac aat	2009
Val Phe Ala Asp Gly Pro Pro Lys His Ala Ile Ala Tyr Asp Asn Asn	
590 595 600	
cac cgc caa gac ttc cat gcc att gtc ccc aac cac att ccg gag gaa	2057
His Arg Gln Asp Phe His Ala Ile Val Pro Asn His Ile Pro Glu Glu	
605 610 615	
tta tat tgg gtt gag gaa gaa cat cag atc ttt aag aca ctt cag gag	2105
Leu Tyr Trp Val Glu Glu Glu His Gln Ile Phe Lys Thr Leu Gln Glu	
620 625 630	
gag aga agg ctt aga gaa gcg gct atg cgt gct aag gtt gaa aaa aca	2153
Glu Arg Arg Leu Arg Glu Ala Ala Met Arg Ala Lys Val Glu Lys Thr	
635 640 645	
gca ctt ctg aaa act gaa aca aag gaa aga act atg aaa tca ttt tta	2201
Ala Leu Leu Lys Thr Glu Thr Lys Glu Arg Thr Met Lys Ser Phe Leu	
650 655 660 665	
ctg tct cag aag cat gta gta tat act gag cct ctt gat atc caa gct	2249
Leu Ser Gln Lys His Val Val Tyr Thr Glu Pro Leu Asp Ile Gln Ala	
670 675 680	
gga agc agc gtc aca gtt tac tat aat ccc gcc aat aca gta ctt aat	2297
Gly Ser Ser Val Thr Val Tyr Tyr Asn Pro Ala Asn Thr Val Leu Asn	
685 690 695	
ggg aaa cct gaa att tgg ttc aga tgt tca ttt aat cgc tgg act cac	2345
Gly Lys Pro Glu Ile Trp Phe Arg Cys Ser Phe Asn Arg Trp Thr His	
700 705 710	
cgc ctg ggt cca ttg cca cct cag aaa atg tcg cct gct gaa aat ggc	2393
Arg Leu Gly Pro Leu Pro Pro Gln Lys Met Ser Pro Ala Glu Asn Gly	
715 720 725	
acc cat gtc aga gca act gtg aag gtt cca ttg gat gca tat atg atg	2441
Thr His Val Arg Ala Thr Val Lys Val Pro Leu Asp Ala Tyr Met Met	
730 735 740 745	
gat ttt gta ttt tcc gag aga gaa gat ggt ggg att ttt gac aat aag	2489
Asp Phe Val Phe Ser Glu Arg Glu Asp Gly Gly Ile Phe Asp Asn Lys	
750 755 760	
agc gga atg gac tat cac ata cct gtg ttt gga gga gtc gct aaa gaa	2537

Ser Gly Met Asp Tyr His Ile Pro Val Phe Gly Gly Val Ala Lys Glu	
765	770 775
cct cca atg cat att gtc cat att gct gtc gaa atg gca cca att gca	2585
Pro Pro Met His Ile Val His Ile Ala Val Glu Met Ala Pro Ile Ala	
780	785 790
aag gtg gga ggc ctt ggt gat gtt gtt act agt ctt tcc cgt gct gtt	2633
Lys Val Gly Gly Leu Gly Asp Val Val Thr Ser Leu Ser Arg Ala Val	
795	800 805
caa gat tta aac cat aat gtg gat att atc tta cct aag tat gac tgt	2681
Gln Asp Leu Asn His Asn Val Asp Ile Ile Leu Pro Lys Tyr Asp Cys	
810	815 820 825
ttg aag atg aat aat gtg aag gac ttt cgg ttt cac aaa aac tac ttt	2729
Leu Lys Met Asn Asn Val Lys Asp Phe Arg Phe His Lys Asn Tyr Phe	
830	835 840
tgg ggt ggg act gaa ata aaa gta tgg ttt gga aag gtg gaa ggt ctc	2777
Trp Gly Gly Thr Glu Ile Lys Val Trp Phe Gly Lys Val Glu Gly Leu	
845	850 855
tcg gtc tat ttt ttg gag cct caa aac ggg tta ttt tcg aaa ggg tgc	2825
Ser Val Tyr Phe Leu Glu Pro Gln Asn Gly Leu Phe Ser Lys Gly Cys	
860	865 870
gtc tat ggt tgt agc aat gat ggt gaa cga ttt ggt ttc ttc tgt cac	2873
Val Tyr Gly Cys Ser Asn Asp Gly Glu Arg Phe Gly Phe Phe Cys His	
875	880 885
gcg gct ttg gag ttt ctt ctg caa ggt gga ttt agt ccg gat atc att	2921
Ala Ala Leu Glu Phe Leu Leu Gln Gly Gly Phe Ser Pro Asp Ile Ile	
890	895 900 905
cat tgc cat gat tgg tct agt gct cct gtt gct tgg ctc ttt aag gaa	2969
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu Phe Lys Glu	
910	915 920
caa tat aca cac tat ggt cta agc aaa tct cgt ata gtc ttc acg ata	3017
Gln Tyr Thr His Tyr Gly Leu Ser Lys Ser Arg Ile Val Phe Thr Ile	
925	930 935
cat aat ctt gaa ttt ggg gca gat ctc att ggg aga gca atg act aac	3065
His Asn Leu Glu Phe Gly Ala Asp Leu Ile Gly Arg Ala Met Thr Asn	
940	945 950
gca gac aaa gct aca aca gtt tca cca act tac tca cag gag gtg tct	3113
Ala Asp Lys Ala Thr Thr Val Ser Pro Thr Tyr Ser Gln Glu Val Ser	
955	960 965
gga aac cct gta att gcg cct cac ctt cac aag ttc cat ggt ata gtg	3161
Gly Asn Pro Val Ile Ala Pro His Leu His Lys Phe His Gly Ile Val	
970	975 980 985
aat ggg att gac cca gat att tgg gat cct tta aac gat aag ttc att	3209
Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro Leu Asn Asp Lys Phe Ile	

990				995				1000				
ccg att ccg tac	acc tca gaa aac gtt	gtt gaa ggc aaa aca	gca	3254								
Pro Ile Pro Tyr	Thr Ser Glu Asn Val	Val Glu Gly Lys Thr	Ala									
1005	1010	1015										
gcc aag gaa gct	ttg cag cga aaa ctt	gga ctg aaa cag gct	gac	3299								
Ala Lys Glu Ala	Leu Gln Arg Lys Leu	Gly Leu Lys Gln Ala	Asp									
1020	1025	1030										
ctt cct ttg gta	gga att atc acc cgc	tta act cac cag aaa	gga	3344								
Leu Pro Leu Val	Gly Ile Ile Thr Arg	Leu Thr His Gln Lys	Gly									
1035	1040	1045										
atc cac ctc att	aaa cat gct att tgg	cgc acc ttg gaa cgg	aac	3389								
Ile His Leu Ile	Lys His Ala Ile Trp	Arg Thr Leu Glu Arg	Asn									
1050	1055	1060										
gga cag gta gtc	ttg ctt ggt tct gct	cct gat cct agg gta	caa	3434								
Gly Gln Val Val	Leu Leu Gly Ser Ala	Pro Asp Pro Arg Val	Gln									
1065	1070	1075										
aac gat ttt gtt	aat ttg gca aat caa	ttg cac tcc aaa tat	aat	3479								
Asn Asp Phe Val	Asn Leu Ala Asn Gln	Leu His Ser Lys Tyr	Asn									
1080	1085	1090										
gac cgc gca cga	ctc tgt cta aca tat	gac gag cca ctt tct	cac	3524								
Asp Arg Ala Arg	Leu Cys Leu Thr Tyr	Asp Glu Pro Leu Ser	His									
1095	1100	1105										
ctg ata tat gct	ggg gct gat ttt att	cta gtt cct tca ata	ttt	3569								
Leu Ile Tyr Ala	Gly Ala Asp Phe Ile	Leu Val Pro Ser Ile	Phe									
1110	1115	1120										
gag cca tgt gga	cta aca caa ctt acc	gct atg aga tat ggt	tca	3614								
Glu Pro Cys Gly	Leu Thr Gln Leu Thr	Ala Met Arg Tyr Gly	Ser									
1125	1130	1135										
att cca gtc gtg	cgt aaa act gga gga	ctt tat gat act gta	ttt	3659								
Ile Pro Val Val	Arg Lys Thr Gly Gly	Leu Tyr Asp Thr Val	Phe									
1140	1145	1150										
gat gtt gac cat	gac aaa gag aga gca	caa cag tgt ggt ctt	gaa	3704								
Asp Val Asp His	Asp Lys Glu Arg Ala	Gln Gln Cys Gly Leu	Glu									
1155	1160	1165										
cca aat gga ttc	agc ttt gat gga gca	gat gct ggc gga gtt	gat	3749								
Pro Asn Gly Phe	Se											